

Sujit Silas Armstrong Suthahar

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EDUCATION

University of California, Los Angeles

M.S. Bioengineering

GPA: 3.97/4.00

Los Angeles, CA

September 2023 – Present

SKILLS

Programming: Proficient in Python, R, Bash/Shell, Go, SQL, JavaScript, C/C++, CSS/HTML, and LaTeX

Software: MS Word, PowerPoint, Excel, Pymol, Linux, Blender, AutoCAD, IBM SPSS, SAS/STATA, Docker, Git

Machine Learning / Deep Learning: TensorFlow, Keras, PyTorch, Scikit-learn, CUDA, TensorLy

Bioinformatics Tools: STAR aligner, Bowtie2, GATK4, SALMON, DESeq2, Seurat, Scanpy, NextFlow, PyMol, BioPython, Bioconductor, PSIPRED, DeepFold, edgeR, dplyr, tidyr, ggplot2, CibersortX, complex heatmaps, seaborn, WGCNA, MiXCR, etc.

WORK EXPERIENCE

UCLA Institute for Society and Genetics

Graduate Student Researcher (GSR)

Los Angeles, CA

September 2023 – Present

- Led comprehensive multi-omics data analyses (RRBS, WGBS, ATAC-seq, RNA-seq) to elucidate the epigenetic effects of environmental toxins, particularly arsenic, making significant contributions to the emerging field of toxicopigenetics.
- Designed and implemented NextFlow pipelines optimized for both local and distributed computing environments, enhancing reproducibility and scalability of bioinformatics workflows.
- Created a user-friendly HTML-based custom bash script generator specifically for nf-core pipelines, empowering non-expert users to effortlessly submit and manage their jobs on high-performance computing clusters.

GRAIL

Computational Biology & Machine Learning Intern

Menlo Park, CA

June 2024 – September 2024

- Jointly optimized classifier features and assay probes, laying the groundwork for a novel false positive analysis, increasing cell-free DNA detection sensitivity for a few early-stage cancer types by 8%.
- Designed and implemented a cross functional annotation toolkit in a CI/CD environment that helps annotate DMRs and with respect to targeted panel regions and genome annotations optimizing feature selection process reducing non-specific features.
- Refactored functions, updated pipelines, and successfully landed two merge requests related to the development of two vignettes and the false positive analysis workflow.

UCLA Biomedical AI Research Lab

Researcher

Los Angeles, CA

September 2023 – June 2024

- Designed and implemented a multiple instance learning deep learning model for thyroid nodule classification, improving sensitivity by 11% and enhancing diagnostic precision for indeterminate cases.
- Leveraged CUDA architecture to optimize and accelerate deep learning model training on GPUs within a High-Performance Computing (HPC) environment, significantly reducing processing time and improving model iteration speed.
- Developed an advanced U-Net classifier featuring enhanced skip connections and integrated image preprocessing techniques achieving improved sensitivity in biopsy needle segmentation problems for medical imaging.

La Jolla Institute for Immunology

Bioinformatics Specialist

San Diego, CA

June 2021 – July 2023

- Statistically analyzed and automated workflows for single-cell RNA-seq, RNA-seq, and CITE-seq data of PBMC samples, using dimensionality reduction algorithms and R/Python packages to develop preprocessing pipelines and multiple algorithms, enhancing efficiency and reproducibility in high-throughput genomic data analysis.
- Developed and applied a computational method to validate and optimize antibody titration concentrations for a panel of 124 antibodies used in CITE-seq experiments, improving the accuracy and reliability of multi-omics data integration.
- Designed and implemented a novel statistical pipeline to analyze T-cell receptor (TCR) repertoire diversity and clonality from TCR sequencing data, contributing to advancements in immunogenomics research.

- Conducted in-depth mRNA transcriptome analysis using R and Python, spearheading an independent research project comparing hESC transcriptomes of differentiating neural crest and ectodermal cells.
- Employed advanced protein modeling tools including Pymol, I-Tasser, PSIPRED, Robetta, and SAVES 6.0 to elucidate DNA-transcription factor (TF) interactions in early development, integrating molecular biology knowledge with computational approaches to gain novel insights.

LEADERSHIP EXPERIENCE

Highlander Union HUB Associate

Riverside, CA
September 2018 – July 2020

- Fostered student success by facilitating access to campus resources, exemplifying a student-centric approach to service.
- Managed space reservations and event coordination, contributing to a vibrant campus community life.
- Collaborated with professional staff to enhance the university's social and recreational offerings, promoting teamwork.

Danish Display Marketing Director

Tamil Nadu, India
August 2020 – January 2021

- Conceptualized and executed a brand re-design, elevating product, and store appeal, driving a 30% increase in revenue.
- Promoted digital marketing efforts, including website optimization and social media engagement, achieving a 46% growth in followers, and improving business visibility.
- Fostered partnerships with influencers and integrated analytic tools to refine marketing campaigns, demonstrating a keen aptitude for brand promotion and business growth.

SELECTED PUBLICATIONS

Armstrong Suthahar SS, Nettersheim FS, Alimadadi A, Wang E, Billitti M, Resto-Trujillo N, Roy P, Hedrick CC, Ley K, Orecchioni M. Olfir2-positive macrophages originate from monocytes proliferate in situ and present a pro-inflammatory foamy-like phenotype. *Cardiovasc Res.* 2024 Sep 4;cvae153. doi: 10.1093/cvr/cvae153. Epub ahead of print. PMID: 39229899.

Armstrong, S. S., Nettersheim, F. S., Durant, C., Blanco-Dominguez, R., Roy, P., Orecchioni, M., Suryawanshi, V., & Ley, K. (2022). Titration of 124 antibodies using CITE-Seq on human PBMCs. *Scientific Reports*, 12(1), Article 1.

Armstrong Suthahar, S. S., ROY, P., Makings, J., & Ley, K. (2023). Identification of apolipoprotein B-reactive CDR3 motifs allow tracking of atherosclerosis-related memory CD4⁺ T cells in multiple donors. *Frontiers in Immunology*, 15, 1302031.

Athreya, S., Melehy, A., **Armstrong Suthahar, S. S.**, Ivezić, V., Radhachandran, A., Sant, V., ... & Speier, W. (2024). Reducing Overtreatment of Indeterminate Thyroid Nodules Using a Multimodal Deep Learning Model. arXiv preprint arXiv:2409.19171.

PROJECTS

- Survival benefit of liver transplant in mechanically ventilated patients.
- tcrDiff – R package for differential T-cell receptor motif analysis.
- R Shiny app for scRNA-seq and RNA-seq data visualization.
- Using machine learning algorithms to predict heart failure based on clinical records.
- U-Net based deep learning model for lung biopsy needle segmentation in CT-scans.

RELEVANT COURSEWORK

Computer Vision, Linear Algebra, Machine Learning and Data Driven Modelling, Signal and Image Processing, Data Structures in Medical Informatics, Natural Language Processing, Deterministic Modelling, Statistical Mechanics, Advanced Statical Methods, Bayesian Statistics

AWARDS & PROFESSIONAL ASSOCIATIONS

UCLA Graduate Student Researcher, American Association of Immunologists Travel Award, Highlander Union Excellence Award, UCR Achievement Scholarship, American Association of Immunologists - *Member*, Graduate Faculty Executive Commission UCLA - *Samueli School of Engineering Representative*, UCLA Venture Accelerator - *Member*